



SEQUENCE LISTING

<110> LEDBETTER, JEFFREY
HAYDEN-LEDBETTER, MARTHA

<120> DNA VACCINES ENCODING ANTIGEN LINKED TO A DOMAIN THAT BINDS CD40

<130> 034474.0003 UTL1

<140> 09/687,864

<141> 2000-10-13

<150> US 60/159,690

<151> 1999-10-14

<160> 29

<170> PatentIn Ver. 3.2

<210> 1

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<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic
oligonucleotide

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cttcga 66

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<223> Description of Artificial Sequence: Synthetic
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<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Primer

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 <223> Description of Artificial Sequence: Primer

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 <223> Description of Artificial Sequence: Primer

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<220>
 <223> Description of Artificial Sequence: Primer

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 <223> Description of Artificial Sequence: Primer

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<210> 11
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<220>
 <223> Description of Artificial Sequence: Primer

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 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 HIV-human fusion construct

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 <222> (73)..(2238)

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 <222> (73)..(1587)
 <223> HIV gp120 allele + (Gly4Ser)3 linker

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 <221> misc_feature
 <222> (1594)..(2238)
 <223> CD154 extracellular domain from amino acids 48-261+Glu
 binds to CD40

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tgg atc tcg gct tcg aga tct atg ctc ctt ggg ata ttg atg atc tgt 99
 Trp Ile Ser Ala Ser Arg Ser Met Leu Leu Gly Ile Leu Met Ile Cys
 -5 -1 1 5

agt gct aca gaa aaa ttg tgg gtc aca gtc tat tat ggg gta cct gtg 147
 Ser Ala Thr Glu Lys Leu Trp Val Thr Val Tyr Tyr Gly Val Pro Val
 10 15 20 25

tgg aga gaa gca acc acc act cta ttt tgt gca tca gat gct aaa gcc 195
 Trp Arg Glu Ala Thr Thr Thr Leu Phe Cys Ala Ser Asp Ala Lys Ala
 30 35 40

tat gat aca gag gta cat aat gtt tgg gcc aca cat gcc tgt gta ccc 243
 Tyr Asp Thr Glu Val His Asn Val Trp Ala Thr His Ala Cys Val Pro
 45 50 55

aca gac ccc aac cca caa gaa gta gta ttg gga aat gtg aca gaa aat 291
 Thr Asp Pro Asn Pro Gln Glu Val Val Leu Gly Asn Val Thr Glu Asn
 60 65 70

ttt aac atg tgg aaa aat aac atg gta gat cag atg cat gag gat ata 339
 Phe Asn Met Trp Lys Asn Asn Met Val Asp Gln Met His Glu Asp Ile
 75 80 85

atc agt tta tgg gat gaa agc cta aag cca tgt gta aaa tta acc cca 387
 Ile Ser Leu Trp Asp Glu Ser Leu Lys Pro Cys Val Lys Leu Thr Pro
 90 95 100 105

ctc tgt gtt act tta aat tgc act aat ttg aat atc act aag aat act 435
 Leu Cys Val Thr Leu Asn Cys Thr Asn Leu Asn Ile Thr Lys Asn Thr
 110 115 120

act aat ccc act agt agc agc tgg gga atg atg gag aaa gga gaa ata	483
Thr Asn Pro Thr Ser Ser Ser Trp Gly Met Met Glu Lys Gly Glu Ile	
125 130 135	
aaa aat tgc tct ttc tat atc acc aca agc ata aga aat aag gta aag	531
Lys Asn Cys Ser Phe Tyr Ile Thr Thr Ser Ile Arg Asn Lys Val Lys	
140 145 150	
aaa gaa tat gca ctt ttt aat aga ctt gat gta gta cca ata gaa aat	579
Lys Glu Tyr Ala Leu Phe Asn Arg Leu Asp Val Val Pro Ile Glu Asn	
155 160 165	
act aat aat act aag tat agg tta ata agt tgt aac acc tca gtc att	627
Thr Asn Asn Thr Lys Tyr Arg Leu Ile Ser Cys Asn Thr Ser Val Ile	
170 175 180 185	
aca cag gcc tgt cca aag gta tcc ttt cag cca att ccc ata cat tat	675
Thr Gln Ala Cys Pro Lys Val Ser Phe Gln Pro Ile Pro Ile His Tyr	
190 195 200	
tgt gtc ccg gct ggg ttt gcg atg cta aag tgt aac aat aag aca ttc	723
Cys Val Pro Ala Gly Phe Ala Met Leu Lys Cys Asn Asn Lys Thr Phe	
205 210 215	
aat gga tca gga cca tgc aca aat gtc agc aca gta caa tgt aca cat	771
Asn Gly Ser Gly Pro Cys Thr Asn Val Ser Thr Val Gln Cys Thr His	
220 225 230	
gga att agg cca gtg gtg tca act caa ctg ctg tta aat ggc agt cta	819
Gly Ile Arg Pro Val Val Ser Thr Gln Leu Leu Leu Asn Gly Ser Leu	
235 240 245	
gca gaa gaa gac ata gta att aga tct gaa aat ttc aca gac aat gct	867
Ala Glu Glu Asp Ile Val Ile Arg Ser Glu Asn Phe Thr Asp Asn Ala	
250 255 260 265	
aaa acc ata ata gta cag cta aat gaa tct gta gta att aat tgt aca	915
Lys Thr Ile Ile Val Gln Leu Asn Glu Ser Val Val Ile Asn Cys Thr	
270 275 280	
aga ccc aac aac aat aca aga aga agg tta tct ata gga cca ggg aga	963
Arg Pro Asn Asn Asn Thr Arg Arg Arg Leu Ser Ile Gly Pro Gly Arg	
285 290 295	
gca ttt tat gca aga aga aac ata ata gga gat ata aga caa gca cat	1011
Ala Phe Tyr Ala Arg Arg Asn Ile Ile Gly Asp Ile Arg Gln Ala His	
300 305 310	
tgt aac att agt aga gca aaa tgg aat aac act tta caa cag ata gtt	1059
Cys Asn Ile Ser Arg Ala Lys Trp Asn Asn Thr Leu Gln Gln Ile Val	
315 320 325	
ata aaa tta aga gaa aaa ttt agg aat aaa aca ata gcc ttt aat caa	1107
Ile Lys Leu Arg Glu Lys Phe Arg Asn Lys Thr Ile Ala Phe Asn Gln	
330 335 340 345	

tcc tca gga ggg gac cca gaa att gta atg cac agt ttt aat tgt gga	1155
Ser Ser Gly Gly Asp Pro Glu Ile Val Met His Ser Phe Asn Cys Gly	
350 355 360	
ggg gaa ttc ttc tac tgt aat aca gca caa ctg ttt aat agt act tgg	1203
Gly Glu Phe Phe Tyr Cys Asn Thr Ala Gln Leu Phe Asn Ser Thr Trp	
365 370 375	
aat gtt act gga ggg aca aat ggc act gaa gga aat gac ata atc aca	1251
Asn Val Thr Gly Gly Thr Asn Gly Thr Glu Gly Asn Asp Ile Ile Thr	
380 385 390	
ctc caa tgc aga ata aaa caa att ata aat atg tgg cag aaa gta gga	1299
Leu Gln Cys Arg Ile Lys Gln Ile Ile Asn Met Trp Gln Lys Val Gly	
395 400 405	
aaa gca atg tat gcc cct ccc atc aca gga caa att aga tgt tca tca	1347
Lys Ala Met Tyr Ala Pro Pro Ile Thr Gly Gln Ile Arg Cys Ser Ser	
410 415 420 425	
aat att aca ggg ctg cta cta aca aga gat gga ggt aat agt act gag	1395
Asn Ile Thr Gly Leu Leu Leu Thr Arg Asp Gly Gly Asn Ser Thr Glu	
430 435 440	
act gag act gag atc ttc aga cct gga gga gga gat atg agg gac aat	1443
Thr Glu Thr Glu Ile Phe Arg Pro Gly Gly Gly Asp Met Arg Asp Asn	
445 450 455	
tgg aga agt gaa tta tat aaa tat aaa gta gta aga att gaa cca ata	1491
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460 465 470	
gga gta gca ccc acc agg gca aag aga aga aca gtg caa aga gaa aaa	1539
Gly Val Ala Pro Thr Arg Ala Lys Arg Arg Thr Val Gln Arg Glu Lys	
475 480 485	
aga ggg gga ggc ggt tca gga ggt gga ggt tct gga ggt ggc gga tcg	1587
Arg Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser	
490 495 500 505	
gat cca aga agg ttg gac aag ata gaa gat gaa agg aat ctt cat gaa	1635
Asp Pro Arg Arg Leu Asp Lys Ile Glu Asp Glu Arg Asn Leu His Glu	
510 515 520	
gat ttt gta ttc atg aaa acg ata cag aga tgc aac aca gga gaa aga	1683
Asp Phe Val Phe Met Lys Thr Ile Gln Arg Cys Asn Thr Gly Glu Arg	
525 530 535	
tcc tta tcc tta ctg aac tgt gag gag att aaa agc cag ttt gaa ggc	1731
Ser Leu Ser Leu Leu Asn Cys Glu Glu Ile Lys Ser Gln Phe Glu Gly	
540 545 550	
ttt gtg aag gat ata atg tta aac aaa gag gag acg aag aaa gaa aac	1779
Phe Val Lys Asp Ile Met Leu Asn Lys Glu Glu Thr Lys Lys Glu Asn	
555 560 565	

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gtc ata agt gag gcc agc agt aaa aca aca tct gtg tta cag tgg gct 1875
Val Ile Ser Glu Ala Ser Ser Lys Thr Thr Ser Val Leu Gln Trp Ala
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gaa aaa gga tac tac acc atg agc aac aac ttg gta acc ctg gaa aat 1923
Glu Lys Gly Tyr Tyr Thr Met Ser Asn Asn Leu Val Thr Leu Glu Asn
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ggg aaa cag ctg acc gtt aaa aga caa gga ctc tat tat atc tat gcc 1971
Gly Lys Gln Leu Thr Val Lys Arg Gln Gly Leu Tyr Tyr Ile Tyr Ala
                               620                               625                               630

caa gtc acc ttc tgt tcc aat cgg gaa gct tcg agt caa gct cca ttt 2019
Gln Val Thr Phe Cys Ser Asn Arg Glu Ala Ser Ser Gln Ala Pro Phe
                               635                               640                               645

ata gcc agc ctc tgc cta aag tcc ccc ggt aga ttc gag aga atc tta 2067
Ile Ala Ser Leu Cys Leu Lys Ser Pro Gly Arg Phe Glu Arg Ile Leu
650                               655                               660                               665

ctc aga gct gca aat acc cac agt tcc gcc aaa cct tgc ggg caa caa 2115
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                               670                               675                               680

tcc att cac ttg gga gga gta ttt gaa ttg caa cca ggt gct tcg gtg 2163
Ser Ile His Leu Gly Gly Val Phe Glu Leu Gln Pro Gly Ala Ser Val
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ttt gtc aat gtg act gat cca agc caa gtg agc cat ggc act ggc ttc 2211
Phe Val Asn Val Thr Asp Pro Ser Gln Val Ser His Gly Thr Gly Phe
                               700                               705                               710

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<210> 13

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<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic
HIV-human fusion construct

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<221> CDS

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 <223> HIV gp120 allele + ProAspPro linker

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 <222> (1552)..(2196)
 <223> CD154 extracellular domain long form (amino acids 48-261)+Glu
 binds to CD40

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agt gct aca gaa aaa ttg tgg gtc aca gtc tat tat ggg gta cct gtg 147
 Ser Ala Thr Glu Lys Leu Trp Val Thr Val Tyr Tyr Gly Val Pro Val
 10 15 20 25

tgg aga gaa gca acc acc act cta ttt tgt gca tca gat gct aaa gcc 195
 Trp Arg Glu Ala Thr Thr Thr Leu Phe Cys Ala Ser Asp Ala Lys Ala
 30 35 40

tat gat aca gag gta cat aat gtt tgg gcc aca cat gcc tgt gta ccc 243
 Tyr Asp Thr Glu Val His Asn Val Trp Ala Thr His Ala Cys Val Pro
 45 50 55

aca gac ccc aac cca caa gaa gta gta ttg gga aat gtg aca gaa aat 291
 Thr Asp Pro Asn Pro Gln Glu Val Val Leu Gly Asn Val Thr Glu Asn
 60 65 70

ttt aac atg tgg aaa aat aac atg gta gat cag atg cat gag gat ata 339
 Phe Asn Met Trp Lys Asn Asn Met Val Asp Gln Met His Glu Asp Ile
 75 80 85

atc agt tta tgg gat gaa agc cta aag cca tgt gta aaa tta acc cca 387
 Ile Ser Leu Trp Asp Glu Ser Leu Lys Pro Cys Val Lys Leu Thr Pro
 90 95 100 105

ctc tgt gtt act tta aat tgc act aat ttg aat atc act aag aat act 435
 Leu Cys Val Thr Leu Asn Cys Thr Asn Leu Asn Ile Thr Lys Asn Thr
 110 115 120

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Thr	Asn	Pro	Thr	Ser	Ser	Ser	Trp	Gly	Met	Met	Glu	Lys	Gly	Glu	Ile	
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aaa	aat	tgc	tct	ttc	tat	atc	acc	aca	agc	ata	aga	aat	aag	gta	aag	531
Lys	Asn	Cys	Ser	Phe	Tyr	Ile	Thr	Thr	Ser	Ile	Arg	Asn	Lys	Val	Lys	
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aaa	gaa	tat	gca	ctt	ttt	aat	aga	ctt	gat	gta	gta	cca	ata	gaa	aat	579
Lys	Glu	Tyr	Ala	Leu	Phe	Asn	Arg	Leu	Asp	Val	Val	Pro	Ile	Glu	Asn	
	155					160					165					
act	aat	aat	act	aag	tat	agg	tta	ata	agt	tgt	aac	acc	tca	gtc	att	627
Thr	Asn	Asn	Thr	Lys	Tyr	Arg	Leu	Ile	Ser	Cys	Asn	Thr	Ser	Val	Ile	
170					175					180					185	
aca	cag	gcc	tgt	cca	aag	gta	tcc	ttt	cag	cca	att	ccc	ata	cat	tat	675
Thr	Gln	Ala	Cys	Pro	Lys	Val	Ser	Phe	Gln	Pro	Ile	Pro	Ile	His	Tyr	
				190					195					200		
tgt	gtc	ccg	gct	ggg	ttt	gcg	atg	cta	aag	tgt	aac	aat	aag	aca	ttc	723
Cys	Val	Pro	Ala	Gly	Phe	Ala	Met	Leu	Lys	Cys	Asn	Asn	Lys	Thr	Phe	
			205					210					215			
aat	gga	tca	gga	cca	tgc	aca	aat	gtc	agc	aca	gta	caa	tgt	aca	cat	771
Asn	Gly	Ser	Gly	Pro	Cys	Thr	Asn	Val	Ser	Thr	Val	Gln	Cys	Thr	His	
		220					225					230				
gga	att	agg	cca	gtg	gtg	tca	act	caa	ctg	ctg	tta	aat	ggc	agt	cta	819
Gly	Ile	Arg	Pro	Val	Val	Ser	Thr	Gln	Leu	Leu	Leu	Asn	Gly	Ser	Leu	
	235					240					245					
gca	gaa	gaa	gac	ata	gta	att	aga	tct	gaa	aat	ttc	aca	gac	aat	gct	867
Ala	Glu	Glu	Asp	Ile	Val	Ile	Arg	Ser	Glu	Asn	Phe	Thr	Asp	Asn	Ala	
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Lys	Thr	Ile	Ile	Val	Gln	Leu	Asn	Glu	Ser	Val	Val	Ile	Asn	Cys	Thr	
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aga	ccc	aac	aac	aat	aca	aga	aga	agg	tta	tct	ata	gga	cca	ggg	aga	963
Arg	Pro	Asn	Asn	Asn	Thr	Arg	Arg	Arg	Leu	Ser	Ile	Gly	Pro	Gly	Arg	
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gca	ttt	tat	gca	aga	aga	aac	ata	ata	gga	gat	ata	aga	caa	gca	cat	1011
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tgt	aac	att	agt	aga	gca	aaa	tgg	aat	aac	act	tta	caa	cag	ata	gtt	1059
Cys	Asn	Ile	Ser	Arg	Ala	Lys	Trp	Asn	Asn	Thr	Leu	Gln	Gln	Ile	Val	
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Ile	Lys	Leu	Arg	Glu	Lys	Phe	Arg	Asn	Lys	Thr	Ile	Ala	Phe	Asn	Gln	
330					335					340					345	

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Ser Ser Gly Gly Asp Pro Glu Ile Val Met His Ser Phe Asn Cys Gly	
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ggg gaa ttc ttc tac tgt aat aca gca caa ctg ttt aat agt act tgg	1203
Gly Glu Phe Phe Tyr Cys Asn Thr Ala Gln Leu Phe Asn Ser Thr Trp	
365 370 375	
aat gtt act gga ggg aca aat ggc act gaa gga aat gac ata atc aca	1251
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380 385 390	
ctc caa tgc aga ata aaa caa att ata aat atg tgg cag aaa gta gga	1299
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395 400 405	
aaa gca atg tat gcc cct ccc atc aca gga caa att aga tgt tca tca	1347
Lys Ala Met Tyr Ala Pro Pro Ile Thr Gly Gln Ile Arg Cys Ser Ser	
410 415 420 425	
aat att aca ggg ctg cta cta aca aga gat gga ggt aat agt act gag	1395
Asn Ile Thr Gly Leu Leu Leu Thr Arg Asp Gly Gly Asn Ser Thr Glu	
430 435 440	
act gag act gag atc ttc aga cct gga gga gga gat atg agg gac aat	1443
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445 450 455	
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Trp Arg Ser Glu Leu Tyr Lys Tyr Lys Val Val Arg Ile Glu Pro Ile	
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Gly Val Ala Pro Thr Arg Ala Lys Arg Arg Thr Val Gln Arg Glu Lys	
475 480 485	
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Arg Pro Asp Pro Arg Arg Leu Asp Lys Ile Glu Asp Glu Arg Asn Leu	
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gaa ggc ttt gtg aag gat ata atg tta aac aaa gag gag acg aag aaa	1731
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590 595 600	
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Glu Asn Gly Lys Gln Leu Thr Val Lys Arg Gln Gly Leu Tyr Tyr Ile	
605 610 615	
tat gcc caa gtc acc ttc tgt tcc aat cgg gaa gct tcg agt caa gct	1971
Tyr Ala Gln Val Thr Phe Cys Ser Asn Arg Glu Ala Ser Ser Gln Ala	
620 625 630	
cca ttt ata gcc agc ctc tgc cta aag tcc ccc ggt aga ttc gag aga	2019
Pro Phe Ile Ala Ser Leu Cys Leu Lys Ser Pro Gly Arg Phe Glu Arg	
635 640 645	
atc tta ctc aga gct gca aat acc cac agt tcc gcc aaa cct tgc ggg	2067
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670 675 680	
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Ser Val Phe Val Asn Val Thr Asp Pro Ser Gln Val Ser His Gly Thr	
685 690 695	
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<210> 14

<211> 2070

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic
HIV-human fusion construct

<220>

<221> CDS

<222> (13)..(2058)

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 <222> (73)..(1587)
 <223> HIV gp120 allele + (Gly4Ser)3 linker

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 <222> (1594)..(2058)
 <223> CD154 extracellular domain from amino acids 108-261+Glu
 binds to CD40

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 aagcttgccg cc atg ctg tat acc tct cag ctg tta gga cta ctt ctg ttt 51
 Met Leu Tyr Thr Ser Gln Leu Leu Gly Leu Leu Leu Phe
 -20 -15 -10

tgg atc tcg gct tcg aga tct atg ctc ctt ggg ata ttg atg atc tgt 99
 Trp Ile Ser Ala Ser Arg Ser Met Leu Leu Gly Ile Leu Met Ile Cys
 -5 -1 1 5

agt gct aca gaa aaa ttg tgg gtc aca gtc tat tat ggg gta cct gtg 147
 Ser Ala Thr Glu Lys Leu Trp Val Thr Val Tyr Tyr Gly Val Pro Val
 10 15 20 25

tgg aga gaa gca acc acc act cta ttt tgt gca tca gat gct aaa gcc 195
 Trp Arg Glu Ala Thr Thr Thr Leu Phe Cys Ala Ser Asp Ala Lys Ala
 30 35 40

tat gat aca gag gta cat aat gtt tgg gcc aca cat gcc tgt gta ccc 243
 Tyr Asp Thr Glu Val His Asn Val Trp Ala Thr His Ala Cys Val Pro
 45 50 55

aca gac ccc aac cca caa gaa gta gta ttg gga aat gtg aca gaa aat 291
 Thr Asp Pro Asn Pro Gln Glu Val Val Leu Gly Asn Val Thr Glu Asn
 60 65 70

ttt aac atg tgg aaa aat aac atg gta gat cag atg cat gag gat ata 339
 Phe Asn Met Trp Lys Asn Asn Met Val Asp Gln Met His Glu Asp Ile
 75 80 85

atc agt tta tgg gat gaa agc cta aag cca tgt gta aaa tta acc cca 387
 Ile Ser Leu Trp Asp Glu Ser Leu Lys Pro Cys Val Lys Leu Thr Pro
 90 95 100 105

ctc tgt gtt act tta aat tgc act aat ttg aat atc act aag aat act 435
 Leu Cys Val Thr Leu Asn Cys Thr Asn Leu Asn Ile Thr Lys Asn Thr
 110 115 120

act aat ccc act agt agc agc tgg gga atg atg gag aaa gga gaa ata 483
 Thr Asn Pro Thr Ser Ser Ser Trp Gly Met Met Glu Lys Gly Glu Ile
 125 130 135

aaa aat tgc tct ttc tat atc acc aca agc ata aga aat aag gta aag	531
Lys Asn Cys Ser Phe Tyr Ile Thr Thr Ser Ile Arg Asn Lys Val Lys	
140 145 150	
aaa gaa tat gca ctt ttt aat aga ctt gat gta gta cca ata gaa aat	579
Lys Glu Tyr Ala Leu Phe Asn Arg Leu Asp Val Val Pro Ile Glu Asn	
155 160 165	
act aat aat act aag tat agg tta ata agt tgt aac acc tca gtc att	627
Thr Asn Asn Thr Lys Tyr Arg Leu Ile Ser Cys Asn Thr Ser Val Ile	
170 175 180 185	
aca cag gcc tgt cca aag gta tcc ttt cag cca att ccc ata cat tat	675
Thr Gln Ala Cys Pro Lys Val Ser Phe Gln Pro Ile Pro Ile His Tyr	
190 195 200	
tgt gtc ccg gct ggg ttt gcg atg cta aag tgt aac aat aag aca ttc	723
Cys Val Pro Ala Gly Phe Ala Met Leu Lys Cys Asn Asn Lys Thr Phe	
205 210 215	
aat gga tca gga cca tgc aca aat gtc agc aca gta caa tgt aca cat	771
Asn Gly Ser Gly Pro Cys Thr Asn Val Ser Thr Val Gln Cys Thr His	
220 225 230	
gga att agg cca gtg gtg tca act caa ctg ctg tta aat ggc agt cta	819
Gly Ile Arg Pro Val Val Ser Thr Gln Leu Leu Leu Asn Gly Ser Leu	
235 240 245	
gca gaa gaa gac ata gta att aga tct gaa aat ttc aca gac aat gct	867
Ala Glu Glu Asp Ile Val Ile Arg Ser Glu Asn Phe Thr Asp Asn Ala	
250 255 260 265	
aaa acc ata ata gta cag cta aat gaa tct gta gta att aat tgt aca	915
Lys Thr Ile Ile Val Gln Leu Asn Glu Ser Val Val Ile Asn Cys Thr	
270 275 280	
aga ccc aac aac aat aca aga aga agg tta tct ata gga cca ggg aga	963
Arg Pro Asn Asn Asn Thr Arg Arg Arg Leu Ser Ile Gly Pro Gly Arg	
285 290 295	
gca ttt tat gca aga aga aac ata ata gga gat ata aga caa gca cat	1011
Ala Phe Tyr Ala Arg Arg Asn Ile Ile Gly Asp Ile Arg Gln Ala His	
300 305 310	
tgt aac att agt aga gca aaa tgg aat aac act tta caa cag ata gtt	1059
Cys Asn Ile Ser Arg Ala Lys Trp Asn Asn Thr Leu Gln Gln Ile Val	
315 320 325	
ata aaa tta aga gaa aaa ttt agg aat aaa aca ata gcc ttt aat caa	1107
Ile Lys Leu Arg Glu Lys Phe Arg Asn Lys Thr Ile Ala Phe Asn Gln	
330 335 340 345	
tcc tca gga ggg gac cca gaa att gta atg cac agt ttt aat tgt gga	1155
Ser Ser Gly Gly Asp Pro Glu Ile Val Met His Ser Phe Asn Cys Gly	
350 355 360	

ggg gaa ttc ttc tac tgt aat aca gca caa ctg ttt aat agt act tgg	1203
Gly Glu Phe Phe Tyr Cys Asn Thr Ala Gln Leu Phe Asn Ser Thr Trp	
365 370 375	
aat gtt act gga ggg aca aat ggc act gaa gga aat gac ata atc aca	1251
Asn Val Thr Gly Gly Thr Asn Gly Thr Glu Gly Asn Asp Ile Ile Thr	
380 385 390	
ctc caa tgc aga ata aaa caa att ata aat atg tgg cag aaa gta gga	1299
Leu Gln Cys Arg Ile Lys Gln Ile Ile Asn Met Trp Gln Lys Val Gly	
395 400 405	
aaa gca atg tat gcc cct ccc atc aca gga caa att aga tgt tca tca	1347
Lys Ala Met Tyr Ala Pro Pro Ile Thr Gly Gln Ile Arg Cys Ser Ser	
410 415 420 425	
aat att aca ggg ctg cta cta aca aga gat gga ggt aat agt act gag	1395
Asn Ile Thr Gly Leu Leu Leu Thr Arg Asp Gly Gly Asn Ser Thr Glu	
430 435 440	
act gag act gag atc ttc aga cct gga gga gga gat atg agg gac aat	1443
Thr Glu Thr Glu Ile Phe Arg Pro Gly Gly Gly Asp Met Arg Asp Asn	
445 450 455	
tgg aga agt gaa tta tat aaa tat aaa gta gta aga att gaa cca ata	1491
Trp Arg Ser Glu Leu Tyr Lys Tyr Lys Val Val Arg Ile Glu Pro Ile	
460 465 470	
gga gta gca ccc acc agg gca aag aga aga aca gtg caa aga gaa aaa	1539
Gly Val Ala Pro Thr Arg Ala Lys Arg Arg Thr Val Gln Arg Glu Lys	
475 480 485	
aga ggg gga ggc ggt tca gga ggt gga ggt tct gga ggt ggc gga tcg	1587
Arg Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser	
490 495 500 505	
gat cca gaa aac agc ttt gaa atg caa aaa ggt gat cag aat cct caa	1635
Asp Pro Glu Asn Ser Phe Glu Met Gln Lys Gly Asp Gln Asn Pro Gln	
510 515 520	
att gcg gca cat gtc ata agt gag gcc agc agt aaa aca aca tct gtg	1683
Ile Ala Ala His Val Ile Ser Glu Ala Ser Ser Lys Thr Thr Ser Val	
525 530 535	
tta cag tgg gct gaa aaa gga tac tac acc atg agc aac aac ttg gta	1731
Leu Gln Trp Ala Glu Lys Gly Tyr Tyr Thr Met Ser Asn Asn Leu Val	
540 545 550	
acc ctg gaa aat ggg aaa cag ctg acc gtt aaa aga caa gga ctc tat	1779
Thr Leu Glu Asn Gly Lys Gln Leu Thr Val Lys Arg Gln Gly Leu Tyr	
555 560 565	
tat atc tat gcc caa gtc acc ttc tgt tcc aat cgg gaa gct tcg agt	1827
Tyr Ile Tyr Ala Gln Val Thr Phe Cys Ser Asn Arg Glu Ala Ser Ser	
570 575 580 585	

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caa gct cca ttt ata gcc agc ctc tgc cta aag tcc ccc ggt aga ttc 1875
Gln Ala Pro Phe Ile Ala Ser Leu Cys Leu Lys Ser Pro Gly Arg Phe
                    590                    595                    600

gag aga atc tta ctc aga gct gca aat acc cac agt tcc gcc aaa cct 1923
Glu Arg Ile Leu Leu Arg Ala Ala Asn Thr His Ser Ser Ala Lys Pro
                    605                    610                    615

tgc ggg caa caa tcc att cac ttg gga gga gta ttt gaa ttg caa cca 1971
Cys Gly Gln Gln Ser Ile His Leu Gly Gly Val Phe Glu Leu Gln Pro
                    620                    625                    630

ggt gct tcg gtg ttt gtc aat gtg act gat cca agc caa gtg agc cat 2019
Gly Ala Ser Val Phe Val Asn Val Thr Asp Pro Ser Gln Val Ser His
                    635                    640                    645

ggc act ggc ttc acg tcc ttt ggc tta ctc aaa ctc gag tgataatcta ga 2070
Gly Thr Gly Phe Thr Ser Phe Gly Leu Leu Lys Leu Glu
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<210> 15
<211> 2028
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      HIV-human fusion construct

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<222> (13)..(72)

<220>
<221> mat_peptide
<222> (73)..(2016)

<220>
<221> misc_feature
<222> (73)..(1551)
<223> HIV gp120 allele + ProAspPro linker

<220>
<221> misc_feature
<222> (1552)..(2016)
<223> CD154 extracellular domain from amino acids 108-261+Glu
      binds to CD40

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      Met Leu Tyr Thr Ser Gln Leu Leu Gly Leu Leu Leu Phe
      -20              -15              -10

tgg atc tcg gct tcg aga tcc atg ctc ctt ggg ata ttg atg atc tgt 99
Trp Ile Ser Ala Ser Arg Ser Met Leu Leu Gly Ile Leu Met Ile Cys
      -5              -1      1              5

agt gct aca gaa aaa ttg tgg gtc aca gtc tat tat ggg gta cct gtg 147
Ser Ala Thr Glu Lys Leu Trp Val Thr Val Tyr Tyr Gly Val Pro Val
      10              15              20              25

tgg aga gaa gca acc acc act cta ttt tgt gca tca gat gct aaa gcc 195
Trp Arg Glu Ala Thr Thr Thr Leu Phe Cys Ala Ser Asp Ala Lys Ala
      30              35              40

tat gat aca gag gta cat aat gtt tgg gcc aca cat gcc tgt gta ccc 243
Tyr Asp Thr Glu Val His Asn Val Trp Ala Thr His Ala Cys Val Pro
      45              50              55

aca gac ccc aac cca caa gaa gta gta ttg gga aat gtg aca gaa aat 291
Thr Asp Pro Asn Pro Gln Glu Val Val Leu Gly Asn Val Thr Glu Asn
      60              65              70

ttt aac atg tgg aaa aat aac atg gta gat cag atg cat gag gat ata 339
Phe Asn Met Trp Lys Asn Asn Met Val Asp Gln Met His Glu Asp Ile
      75              80              85

atc agt tta tgg gat gaa agc cta aag cca tgt gta aaa tta acc cca 387
Ile Ser Leu Trp Asp Glu Ser Leu Lys Pro Cys Val Lys Leu Thr Pro
      90              95              100              105

ctc tgt gtt act tta aat tgc act aat ttg aat atc act aag aat act 435
Leu Cys Val Thr Leu Asn Cys Thr Asn Leu Asn Ile Thr Lys Asn Thr
      110              115              120

act aat ccc act agt agc agc tgg gga atg atg gag aaa gga gaa ata 483
Thr Asn Pro Thr Ser Ser Ser Trp Gly Met Met Glu Lys Gly Glu Ile
      125              130              135

aaa aat tgc tct ttc tat atc acc aca agc ata aga aat aag gta aag 531
Lys Asn Cys Ser Phe Tyr Ile Thr Thr Ser Ile Arg Asn Lys Val Lys
      140              145              150

aaa gaa tat gca ctt ttt aat aga ctt gat gta gta cca ata gaa aat 579
Lys Glu Tyr Ala Leu Phe Asn Arg Leu Asp Val Val Pro Ile Glu Asn
      155              160              165

act aat aat act aag tat agg tta ata agt tgt aac acc tca gtc att 627
Thr Asn Asn Thr Lys Tyr Arg Leu Ile Ser Cys Asn Thr Ser Val Ile
      170              175              180              185

aca cag gcc tgt cca aag gta tcc ttt cag cca att ccc ata cat tat 675
Thr Gln Ala Cys Pro Lys Val Ser Phe Gln Pro Ile Pro Ile His Tyr
      190              195              200

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tgt gtc ccg gct ggg ttt gcg atg cta aag tgt aac aat aag aca ttc	723
Cys Val Pro Ala Gly Phe Ala Met Leu Lys Cys Asn Asn Lys Thr Phe	
205 210 215	
aat gga tca gga cca tgc aca aat gtc agc aca gta caa tgt aca cat	771
Asn Gly Ser Gly Pro Cys Thr Asn Val Ser Thr Val Gln Cys Thr His	
220 225 230	
gga att agg cca gtg gtg tca act caa ctg ctg tta aat ggc agt cta	819
Gly Ile Arg Pro Val Val Ser Thr Gln Leu Leu Leu Asn Gly Ser Leu	
235 240 245	
gca gaa gaa gac ata gta att aga tct gaa aat ttc aca gac aat gct	867
Ala Glu Glu Asp Ile Val Ile Arg Ser Glu Asn Phe Thr Asp Asn Ala	
250 255 260 265	
aaa acc ata ata gta cag cta aat gaa tct gta gta att aat tgt aca	915
Lys Thr Ile Ile Val Gln Leu Asn Glu Ser Val Val Ile Asn Cys Thr	
270 275 280	
aga ccc aac aac aat aca aga aga agg tta tct ata gga cca ggg aga	963
Arg Pro Asn Asn Asn Thr Arg Arg Arg Leu Ser Ile Gly Pro Gly Arg	
285 290 295	
gca ttt tat gca aga aga aac ata ata gga gat ata aga caa gca cat	1011
Ala Phe Tyr Ala Arg Arg Asn Ile Ile Gly Asp Ile Arg Gln Ala His	
300 305 310	
tgt aac att agt aga gca aaa tgg aat aac act tta caa cag ata gtt	1059
Cys Asn Ile Ser Arg Ala Lys Trp Asn Asn Thr Leu Gln Gln Ile Val	
315 320 325	
ata aaa tta aga gaa aaa ttt agg aat aaa aca ata gcc ttt aat caa	1107
Ile Lys Leu Arg Glu Lys Phe Arg Asn Lys Thr Ile Ala Phe Asn Gln	
330 335 340 345	
tcc tca gga ggg gac cca gaa att gta atg cac agt ttt aat tgt gga	1155
Ser Ser Gly Gly Asp Pro Glu Ile Val Met His Ser Phe Asn Cys Gly	
350 355 360	
ggg gaa ttc ttc tac tgt aat aca gca caa ctg ttt aat agt act tgg	1203
Gly Glu Phe Phe Tyr Cys Asn Thr Ala Gln Leu Phe Asn Ser Thr Trp	
365 370 375	
aat gtt act gga ggg aca aat ggc act gaa gga aat gac ata atc aca	1251
Asn Val Thr Gly Gly Thr Asn Gly Thr Glu Gly Asn Asp Ile Ile Thr	
380 385 390	
ctc caa tgc aga ata aaa caa att ata aat atg tgg cag aaa gta gga	1299
Leu Gln Cys Arg Ile Lys Gln Ile Ile Asn Met Trp Gln Lys Val Gly	
395 400 405	
aaa gca atg tat gcc cct ccc atc aca gga caa att aga tgt tca tca	1347
Lys Ala Met Tyr Ala Pro Pro Ile Thr Gly Gln Ile Arg Cys Ser Ser	
410 415 420 425	

aat att aca ggg ctg cta cta aca aga gat gga ggt aat agt act gag	1395
Asn Ile Thr Gly Leu Leu Leu Thr Arg Asp Gly Gly Asn Ser Thr Glu	
430 435 440	
act gag act gag atc ttc aga cct gga gga gga gat atg agg gac aat	1443
Thr Glu Thr Glu Ile Phe Arg Pro Gly Gly Gly Asp Met Arg Asp Asn	
445 450 455	
tgg aga agt gaa tta tat aaa tat aaa gta gta aga att gaa cca ata	1491
Trp Arg Ser Glu Leu Tyr Lys Tyr Lys Val Val Arg Ile Glu Pro Ile	
460 465 470	
gga gta gca ccc acc agg gca aag aga aga aca gtg caa aga gaa aaa	1539
Gly Val Ala Pro Thr Arg Ala Lys Arg Arg Thr Val Gln Arg Glu Lys	
475 480 485	
aga ccg gat cca gaa aac agc ttt gaa atg caa aaa ggt gat cag aat	1587
Arg Pro Asp Pro Glu Asn Ser Phe Glu Met Gln Lys Gly Asp Gln Asn	
490 495 500 505	
cct caa att gcg gca cat gtc ata agt gag gcc agc agt aaa aca aca	1635
Pro Gln Ile Ala Ala His Val Ile Ser Glu Ala Ser Ser Lys Thr Thr	
510 515 520	
tct gtg tta cag tgg gct gaa aaa gga tac tac acc atg agc aac aac	1683
Ser Val Leu Gln Trp Ala Glu Lys Gly Tyr Tyr Thr Met Ser Asn Asn	
525 530 535	
ttg gta acc ctg gaa aat ggg aaa cag ctg acc gtt aaa aga caa gga	1731
Leu Val Thr Leu Glu Asn Gly Lys Gln Leu Thr Val Lys Arg Gln Gly	
540 545 550	
ctc tat tat atc tat gcc caa gtc acc ttc tgt tcc aat cgg gaa gct	1779
Leu Tyr Tyr Ile Tyr Ala Gln Val Thr Phe Cys Ser Asn Arg Glu Ala	
555 560 565	
tcg agt caa gct cca ttt ata gcc agc ctc tgc cta aag tcc ccc ggt	1827
Ser Ser Gln Ala Pro Phe Ile Ala Ser Leu Cys Leu Lys Ser Pro Gly	
570 575 580 585	
aga ttc gag aga atc tta ctc aga gct gca aat acc cac agt tcc gcc	1875
Arg Phe Glu Arg Ile Leu Leu Arg Ala Ala Asn Thr His Ser Ser Ala	
590 595 600	
aaa cct tgc ggg caa caa tcc att cac ttg gga gga gta ttt gaa ttg	1923
Lys Pro Cys Gly Gln Gln Ser Ile His Leu Gly Gly Val Phe Glu Leu	
605 610 615	
caa cca ggt gct tcg gtg ttt gtc aat gtg act gat cca agc caa gtg	1971
Gln Pro Gly Ala Ser Val Phe Val Asn Val Thr Asp Pro Ser Gln Val	
620 625 630	
agc cat ggc act ggc ttc acg tcc ttt ggc tta ctc aaa ctc gag	2016
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635 640 645	
tgataatcta ga	2028

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<220>
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 HIV-human fusion construct

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<220>
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 <222> (73)..(894)

<220>
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 <222> (73)..(243)
 <223> HIV gp120 V3 loop + (Gly4Ser)3 linker

<220>
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 <222> (250)..(894)
 <223> CD154 extracellular domain from amino acids 48-261+Glu
 binds to CD40

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 Trp Ile Ser Ala Ser Arg Ser Val Val Ile Asn Cys Thr Arg Pro Asn
 -5 -1 1 5

aac aat aca aga aga agg tta tct ata gga cca ggg aga gca ttt tat 147
 Asn Asn Thr Arg Arg Arg Leu Ser Ile Gly Pro Gly Arg Ala Phe Tyr
 10 15 20 25

gca aga aga aac ata ata gga gat ata aga caa gca cat tgt aac att 195
 Ala Arg Arg Asn Ile Ile Gly Asp Ile Arg Gln Ala His Cys Asn Ile
 30 35 40

agt ggt ggc ggt ggc tca gga ggc ggt gga tct ggc ggt gga ggt tcg 243
 Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
 45 50 55

gat cca aga agg ttg gac aag ata gaa gat gaa agg aat ctt cat gaa	291
Asp Pro Arg Arg Leu Asp Lys Ile Glu Asp Glu Arg Asn Leu His Glu	
60 65 70	
gat ttt gta ttc atg aaa acg ata cag aga tgc aac aca gga gaa aga	339
Asp Phe Val Phe Met Lys Thr Ile Gln Arg Cys Asn Thr Gly Glu Arg	
75 80 85	
tcc tta tcc tta ctg aac tgt gag gag att aaa agc cag ttt gaa ggc	387
Ser Leu Ser Leu Leu Asn Cys Glu Glu Ile Lys Ser Gln Phe Glu Gly	
90 95 100 105	
ttt gtg aag gat ata atg tta aac aaa gag gag acg aag aaa gaa aac	435
Phe Val Lys Asp Ile Met Leu Asn Lys Glu Glu Thr Lys Lys Glu Asn	
110 115 120	
agc ttt gaa atg caa aaa ggt gat cag aat cct caa att gcg gca cat	483
Ser Phe Glu Met Gln Lys Gly Asp Gln Asn Pro Gln Ile Ala Ala His	
125 130 135	
gtc ata agt gag gcc agc agt aaa aca aca tct gtg tta cag tgg gct	531
Val Ile Ser Glu Ala Ser Ser Lys Thr Thr Ser Val Leu Gln Trp Ala	
140 145 150	
gaa aaa gga tac tac acc atg agc aac aac ttg gta acc ctg gaa aat	579
Glu Lys Gly Tyr Tyr Thr Met Ser Asn Asn Leu Val Thr Leu Glu Asn	
155 160 165	
ggg aaa cag ctg acc gtt aaa aga caa gga ctc tat tat atc tat gcc	627
Gly Lys Gln Leu Thr Val Lys Arg Gln Gly Leu Tyr Tyr Ile Tyr Ala	
170 175 180 185	
caa gtc acc ttc tgt tcc aat cgg gaa gct tcg agt caa gct cca ttt	675
Gln Val Thr Phe Cys Ser Asn Arg Glu Ala Ser Ser Gln Ala Pro Phe	
190 195 200	
ata gcc agc ctc tgc cta aag tcc ccc ggt aga ttc gag aga atc tta	723
Ile Ala Ser Leu Cys Leu Lys Ser Pro Gly Arg Phe Glu Arg Ile Leu	
205 210 215	
ctc aga gct gca aat acc cac agt tcc gcc aaa cct tgc ggg caa caa	771
Leu Arg Ala Ala Asn Thr His Ser Ser Ala Lys Pro Cys Gly Gln Gln	
220 225 230	
tcc att cac ttg gga gga gta ttt gaa ttg caa cca ggt gct tcg gtg	819
Ser Ile His Leu Gly Gly Val Phe Glu Leu Gln Pro Gly Ala Ser Val	
235 240 245	
ttt gtc aat gtg act gat cca agc caa gtg agc cat ggc act ggc ttc	867
Phe Val Asn Val Thr Asp Pro Ser Gln Val Ser His Gly Thr Gly Phe	
250 255 260 265	
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270	

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		-20					-15					-10				
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Trp	Ile	Ser	Ala	Ser	Arg	Ser	Val	Val	Ile	Asn	Cys	Thr	Arg	Pro	Asn	
		-5				-1	1				5					
aac	aat	aca	aga	aga	agg	tta	tct	ata	gga	cca	ggg	aga	gca	ttt	tat	147
Asn	Asn	Thr	Arg	Arg	Arg	Leu	Ser	Ile	Gly	Pro	Gly	Arg	Ala	Phe	Tyr	
10					15					20				25		
gca	aga	aga	aac	ata	ata	gga	gat	ata	aga	caa	gca	cat	tgt	aac	att	195
Ala	Arg	Arg	Asn	Ile	Ile	Gly	Asp	Ile	Arg	Gln	Ala	His	Cys	Asn	Ile	
				30					35					40		
agt	ccg	gat	cca	aga	agg	ttg	gac	aag	ata	gaa	gat	gaa	agg	aat	ctt	243
Ser	Pro	Asp	Pro	Arg	Arg	Leu	Asp	Lys	Ile	Glu	Asp	Glu	Arg	Asn	Leu	
			45					50					55			
cat	gaa	gat	ttt	gta	ttc	atg	aaa	acg	ata	cag	aga	tgc	aac	aca	gga	291
His	Glu	Asp	Phe	Val	Phe	Met	Lys	Thr	Ile	Gln	Arg	Cys	Asn	Thr	Gly	
		60					65					70				

gaa aga tcc tta tcc tta ctg aac tgt gag gag att aaa agc cag ttt	339
Glu Arg Ser Leu Ser Leu Leu Asn Cys Glu Glu Ile Lys Ser Gln Phe	
75 80 85	
gaa ggc ttt gtg aag gat ata atg tta aac aaa gag gag acg aag aaa	387
Glu Gly Phe Val Lys Asp Ile Met Leu Asn Lys Glu Glu Thr Lys Lys	
90 95 100 105	
gaa aac agc ttt gaa atg caa aaa ggt gat cag aat cct caa att gcg	435
Glu Asn Ser Phe Glu Met Gln Lys Gly Asp Gln Asn Pro Gln Ile Ala	
110 115 120	
gca cat gtc ata agt gag gcc agc agt aaa aca aca tct gtg tta cag	483
Ala His Val Ile Ser Glu Ala Ser Ser Lys Thr Thr Ser Val Leu Gln	
125 130 135	
tgg gct gaa aaa gga tac tac acc atg agc aac aac ttg gta acc ctg	531
Trp Ala Glu Lys Gly Tyr Tyr Thr Met Ser Asn Asn Leu Val Thr Leu	
140 145 150	
gaa aat ggg aaa cag ctg acc gtt aaa aga caa gga ctc tat tat atc	579
Glu Asn Gly Lys Gln Leu Thr Val Lys Arg Gln Gly Leu Tyr Tyr Ile	
155 160 165	
tat gcc caa gtc acc ttc tgt tcc aat cgg gaa gct tcg agt caa gct	627
Tyr Ala Gln Val Thr Phe Cys Ser Asn Arg Glu Ala Ser Ser Gln Ala	
170 175 180 185	
cca ttt ata gcc agc ctc tgc cta aag tcc ccc ggt aga ttc gag aga	675
Pro Phe Ile Ala Ser Leu Cys Leu Lys Ser Pro Gly Arg Phe Glu Arg	
190 195 200	
atc tta ctc aga gct gca aat acc cac agt tcc gcc aaa cct tgc ggg	723
Ile Leu Leu Arg Ala Ala Asn Thr His Ser Ser Ala Lys Pro Cys Gly	
205 210 215	
caa caa tcc att cac ttg gga gga gta ttt gaa ttg caa cca ggt gct	771
Gln Gln Ser Ile His Leu Gly Gly Val Phe Glu Leu Gln Pro Gly Ala	
220 225 230	
tcg gtg ttt gtc aat gtg act gat cca agc caa gtg agc cat ggc act	819
Ser Val Phe Val Asn Val Thr Asp Pro Ser Gln Val Ser His Gly Thr	
235 240 245	
ggc ttc acg tcc ttt ggc tta ctc aaa ctc gag tgataatcta ga	864
Gly Phe Thr Ser Phe Gly Leu Leu Lys Leu Glu	
250 255 260	

<210> 18

<211> 726

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
HIV-human fusion construct

<220>

<221> CDS

<222> (13)..(714)

<220>

<221> sig_peptide

<222> (13)..(72)

<220>

<221> mat_peptide

<222> (73)..(714)

<220>

<221> misc_feature

<222> (73)..(207)

<223> HIV gp120 V3 loop + ProAspPro linker

<220>

<221> misc_feature

<222> (208)..(714)

<223> CD154 extracellular domain from amino acids 108-261+Glu
binds to CD40

<400> 18

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aagcttgccg cc atg ctg tat acc tct cag ctg tta gga cta ctt ctg ttt 51
      Met Leu Tyr Thr Ser Gln Leu Leu Gly Leu Leu Leu Phe
      -20              -15              -10

tgg atc tcg gct tcg aga tct gta gta att aat tgt aca aga ccc aac    99
Trp Ile Ser Ala Ser Arg Ser Val Val Ile Asn Cys Thr Arg Pro Asn
      -5              -1    1              5

aac aat aca aga aga agg tta tct ata gga cca ggg aga gca ttt tat    147
Asn Asn Thr Arg Arg Arg Leu Ser Ile Gly Pro Gly Arg Ala Phe Tyr
      10              15              20              25

gca aga aga aac ata ata gga gat ata aga caa gca cat tgt aac att    195
Ala Arg Arg Asn Ile Ile Gly Asp Ile Arg Gln Ala His Cys Asn Ile
      30              35              40

agt ggt ggc ggt ggc tca gga ggc ggt gga tct ggc ggt gga ggt tcg    243
Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
      45              50              55

gat cca gaa aac agc ttt gaa atg caa aaa ggt gat cag aat cct caa    291
Asp Pro Glu Asn Ser Phe Glu Met Gln Lys Gly Asp Gln Asn Pro Gln
      60              65              70

att gcg gca cat gtc ata agt gag gcc agc agt aaa aca aca tct gtg    339
Ile Ala Ala His Val Ile Ser Glu Ala Ser Ser Lys Thr Thr Ser Val
      75              80              85

```

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tta cag tgg gct gaa aaa gga tac tac acc atg agc aac aac ttg gta 387
Leu Gln Trp Ala Glu Lys Gly Tyr Tyr Thr Met Ser Asn Asn Leu Val
 90                      95                      100                      105

acc ctg gaa aat ggg aaa cag ctg acc gtt aaa aga caa gga ctc tat 435
Thr Leu Glu Asn Gly Lys Gln Leu Thr Val Lys Arg Gln Gly Leu Tyr
                      110                      115                      120

tat atc tat gcc caa gtc acc ttc tgt tcc aat cgg gaa gct tcg agt 483
Tyr Ile Tyr Ala Gln Val Thr Phe Cys Ser Asn Arg Glu Ala Ser Ser
                      125                      130                      135

caa gct cca ttt ata gcc agc ctc tgc cta aag tcc ccc ggt aga ttc 531
Gln Ala Pro Phe Ile Ala Ser Leu Cys Leu Lys Ser Pro Gly Arg Phe
                      140                      145                      150

gag aga atc tta ctc aga gct gca aat acc cac agt tcc gcc aaa cct 579
Glu Arg Ile Leu Leu Arg Ala Ala Asn Thr His Ser Ser Ala Lys Pro
                      155                      160                      165

tgc ggg caa caa tcc att cac ttg gga gga gta ttt gaa ttg caa cca 627
Cys Gly Gln Gln Ser Ile His Leu Gly Gly Val Phe Glu Leu Gln Pro
170                      175                      180                      185

ggt gct tcg gtg ttt gtc aat gtg act gat cca agc caa gtg agc cat 675
Gly Ala Ser Val Phe Val Asn Val Thr Asp Pro Ser Gln Val Ser His
                      190                      195                      200

ggc act ggc ttc acg tcc ttt ggc tta ctc aaa ctc gag tgataatcta ga 726
Gly Thr Gly Phe Thr Ser Phe Gly Leu Leu Lys Leu Glu
                      205                      210

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<210> 19

<211> 684

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
HIV-human fusion construct

<220>

<221> CDS

<222> (13)..(672)

<220>

<221> sig_peptide

<222> (13)..(72)

<220>

<221> mat_peptide

<222> (73)..(672)


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<220>
<221> misc_feature
<222> (208)..(672)
<223> CD154 extracellular domain from amino acids 108-261+Glu
      binds to CD40
```

<400> 19																		
aagc	ttg	ccg	cc	atg	ctg	tat	acc	tct	cag	ctg	tta	gga	cta	ctt	ctg	ttt	51	
				Met	Leu	Tyr	Thr	Ser	Gln	Leu	Leu	Gly	Leu	Leu	Leu	Phe		
				-20					-15					-10				
tgg	atc	tcg	gct	tcg	aga	tct	gta	gta	att	aat	tgt	aca	aga	ccc	aac		99	
Trp	Ile	Ser	Ala	Ser	Arg	Ser	Val	Val	Ile	Asn	Cys	Thr	Arg	Pro	Asn			
				-5					-1	1					5			
aac	aat	aca	aga	aga	agg	tta	tct	ata	gga	cca	ggg	aga	gca	ttt	tat		147	
Asn	Asn	Thr	Arg	Arg	Arg	Leu	Ser	Ile	Gly	Pro	Gly	Arg	Ala	Phe	Tyr			
10					15					20					25			
gca	aga	aga	aac	ata	ata	gga	gat	ata	aga	caa	gca	cat	tgt	aac	att		195	
Ala	Arg	Arg	Asn	Ile	Ile	Gly	Asp	Ile	Arg	Gln	Ala	His	Cys	Asn	Ile			
				30					35					40				
agt	ccg	gat	cca	gaa	aac	agc	ttt	gaa	atg	caa	aaa	ggg	gat	cag	aat		243	
Ser	Pro	Asp	Pro	Glu	Asn	Ser	Phe	Glu	Met	Gln	Lys	Gly	Asp	Gln	Asn			
				45					50					55				
cct	caa	att	gcg	gca	cat	gtc	ata	agt	gag	gcc	agc	agt	aaa	aca	aca		291	
Pro	Gln	Ile	Ala	Ala	His	Val	Ile	Ser	Glu	Ala	Ser	Ser	Lys	Thr	Thr			
				60					65					70				
tct	gtg	tta	cag	tgg	gct	gaa	aaa	gga	tac	tac	acc	atg	agc	aac	aac		339	
Ser	Val	Leu	Gln	Trp	Ala	Glu	Lys	Gly	Tyr	Tyr	Thr	Met	Ser	Asn	Asn			
				75					80					85				
ttg	gta	acc	ctg	gaa	aat	ggg	aaa	cag	ctg	acc	gtt	aaa	aga	caa	gga		387	
Leu	Val	Thr	Leu	Glu	Asn	Gly	Lys	Gln	Leu	Thr	Val	Lys	Arg	Gln	Gly			
90					95					100					105			
ctc	tat	tat	atc	tat	gcc	caa	gtc	acc	ttc	tgt	tcc	aat	cgg	gaa	gct		435	
Leu	Tyr	Tyr	Ile	Tyr	Ala	Gln	Val	Thr	Phe	Cys	Ser	Asn	Arg	Glu	Ala			
				110					115					120				
tcg	agt	caa	gct	cca	ttt	ata	gcc	agc	ctc	tgc	cta	aag	tcc	ccc	ggg		483	
Ser	Ser	Gln	Ala	Pro	Phe	Ile	Ala	Ser	Leu	Cys	Leu	Lys	Ser	Pro	Gly			
				125					130					135				
aga	ttc	gag	aga	atc	tta	ctc	aga	gct	gca	aat	acc	cac	agt	tcc	gcc		531	
Arg	Phe	Glu	Arg	Ile	Leu	Leu	Arg	Ala	Ala	Asn	Thr	His	Ser	Ser	Ala			
				140					145					150				

```

aaa cct tgc ggg caa caa tcc att cac ttg gga gga gta ttt gaa ttg 579
Lys Pro Cys Gly Gln Gln Ser Ile His Leu Gly Gly Val Phe Glu Leu
155 160 165

```

```

caa cca ggt gct tcg gtg ttt gtc aat gtg act gat cca agc caa gtg 627
Gln Pro Gly Ala Ser Val Phe Val Asn Val Thr Asp Pro Ser Gln Val
170 175 180 185

```

```

agc cat ggc act ggc ttc acg tcc ttt ggc tta ctc aaa ctc gag 672
Ser His Gly Thr Gly Phe Thr Ser Phe Gly Leu Leu Lys Leu Glu
190 195 200

```

```

tgataatcta ga 684

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<210> 20

<211> 742

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
HIV-human fusion construct

<220>

<221> SIGNAL

<222> (1)..(20)

<223> Synthetic secretory signal peptide

<220>

<221> DOMAIN

<222> (21)..(526)

<223> HIV gp120 domain with (Gly4Ser)3 linker

<220>

<221> BINDING

<222> (529)..(742)

<223> CD154 extracellular domain long form amino acids 48(Arg) to
261(Leu) + Glu binds CD40

<400> 20

```

Met Leu Tyr Thr Ser Gln Leu Leu Gly Leu Leu Leu Phe Trp Ile Ser
-20 -15 -10 -5

```

```

Ala Ser Arg Ser Met Leu Leu Gly Ile Leu Met Ile Cys Ser Ala Thr
-1 1 5 10

```

```

Glu Lys Leu Trp Val Thr Val Tyr Tyr Gly Val Pro Val Trp Arg Glu
15 20 25

```

```

Ala Thr Thr Thr Leu Phe Cys Ala Ser Asp Ala Lys Ala Tyr Asp Thr
30 35 40

```

```

Glu Val His Asn Val Trp Ala Thr His Ala Cys Val Pro Thr Asp Pro
45 50 55 60

```

Asn	Pro	Gln	Glu	Val	Val	Leu	Gly	Asn	Val	Thr	Glu	Asn	Phe	Asn	Met	65	70	75
Trp	Lys	Asn	Asn	Met	Val	Asp	Gln	Met	His	Glu	Asp	Ile	Ile	Ser	Leu	80	85	90
Trp	Asp	Glu	Ser	Leu	Lys	Pro	Cys	Val	Lys	Leu	Thr	Pro	Leu	Cys	Val	95	100	105
Thr	Leu	Asn	Cys	Thr	Asn	Leu	Asn	Ile	Thr	Lys	Asn	Thr	Thr	Asn	Pro	110	115	120
Thr	Ser	Ser	Ser	Trp	Gly	Met	Met	Glu	Lys	Gly	Glu	Ile	Lys	Asn	Cys	125	130	135
Ser	Phe	Tyr	Ile	Thr	Thr	Ser	Ile	Arg	Asn	Lys	Val	Lys	Lys	Glu	Tyr	145	150	155
Ala	Leu	Phe	Asn	Arg	Leu	Asp	Val	Val	Pro	Ile	Glu	Asn	Thr	Asn	Asn	160	165	170
Thr	Lys	Tyr	Arg	Leu	Ile	Ser	Cys	Asn	Thr	Ser	Val	Ile	Thr	Gln	Ala	175	180	185
Cys	Pro	Lys	Val	Ser	Phe	Gln	Pro	Ile	Pro	Ile	His	Tyr	Cys	Val	Pro	190	195	200
Ala	Gly	Phe	Ala	Met	Leu	Lys	Cys	Asn	Asn	Lys	Thr	Phe	Asn	Gly	Ser	205	210	215
Gly	Pro	Cys	Thr	Asn	Val	Ser	Thr	Val	Gln	Cys	Thr	His	Gly	Ile	Arg	225	230	235
Pro	Val	Val	Ser	Thr	Gln	Leu	Leu	Leu	Asn	Gly	Ser	Leu	Ala	Glu	Glu	240	245	250
Asp	Ile	Val	Ile	Arg	Ser	Glu	Asn	Phe	Thr	Asp	Asn	Ala	Lys	Thr	Ile	255	260	265
Ile	Val	Gln	Leu	Asn	Glu	Ser	Val	Val	Ile	Asn	Cys	Thr	Arg	Pro	Asn	270	275	280
Asn	Asn	Thr	Arg	Arg	Arg	Leu	Ser	Ile	Gly	Pro	Gly	Arg	Ala	Phe	Tyr	285	290	295
Ala	Arg	Arg	Asn	Ile	Ile	Gly	Asp	Ile	Arg	Gln	Ala	His	Cys	Asn	Ile	305	310	315
Ser	Arg	Ala	Lys	Trp	Asn	Asn	Thr	Leu	Gln	Gln	Ile	Val	Ile	Lys	Leu	320	325	330
Arg	Glu	Lys	Phe	Arg	Asn	Lys	Thr	Ile	Ala	Phe	Asn	Gln	Ser	Ser	Gly	335	340	345
Gly	Asp	Pro	Glu	Ile	Val	Met	His	Ser	Phe	Asn	Cys	Gly	Gly	Glu	Phe	350	355	360

Phe Tyr Cys Asn Thr Ala Gln Leu Phe Asn Ser Thr Trp Asn Val Thr
 365 370 375 380
 Gly Gly Thr Asn Gly Thr Glu Gly Asn Asp Ile Ile Thr Leu Gln Cys
 385 390 395
 Arg Ile Lys Gln Ile Ile Asn Met Trp Gln Lys Val Gly Lys Ala Met
 400 405 410
 Tyr Ala Pro Pro Ile Thr Gly Gln Ile Arg Cys Ser Ser Asn Ile Thr
 415 420 425
 Gly Leu Leu Leu Thr Arg Asp Gly Gly Asn Ser Thr Glu Thr Glu Thr
 430 435 440
 Glu Ile Phe Arg Pro Gly Gly Gly Asp Met Arg Asp Asn Trp Arg Ser
 445 450 455 460
 Glu Leu Tyr Lys Tyr Lys Val Val Arg Ile Glu Pro Ile Gly Val Ala
 465 470 475
 Pro Thr Arg Ala Lys Arg Arg Thr Val Gln Arg Glu Lys Arg Gly Gly
 480 485 490
 Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Pro Arg
 495 500 505
 Arg Leu Asp Lys Ile Glu Asp Glu Arg Asn Leu His Glu Asp Phe Val
 510 515 520
 Phe Met Lys Thr Ile Gln Arg Cys Asn Thr Gly Glu Arg Ser Leu Ser
 525 530 535 540
 Leu Leu Asn Cys Glu Glu Ile Lys Ser Gln Phe Glu Gly Phe Val Lys
 545 550 555
 Asp Ile Met Leu Asn Lys Glu Glu Thr Lys Lys Glu Asn Ser Phe Glu
 560 565 570
 Met Gln Lys Gly Asp Gln Asn Pro Gln Ile Ala Ala His Val Ile Ser
 575 580 585
 Glu Ala Ser Ser Lys Thr Thr Ser Val Leu Gln Trp Ala Glu Lys Gly
 590 595 600
 Tyr Tyr Thr Met Ser Asn Asn Leu Val Thr Leu Glu Asn Gly Lys Gln
 605 610 615 620
 Leu Thr Val Lys Arg Gln Gly Leu Tyr Tyr Ile Tyr Ala Gln Val Thr
 625 630 635
 Phe Cys Ser Asn Arg Glu Ala Ser Ser Gln Ala Pro Phe Ile Ala Ser
 640 645 650
 Leu Cys Leu Lys Ser Pro Gly Arg Phe Glu Arg Ile Leu Leu Arg Ala
 655 660 665

Ala Asn Thr His Ser Ser Ala Lys Pro Cys Gly Gln Gln Ser Ile His
670 675 680

Leu Gly Gly Val Phe Glu Leu Gln Pro Gly Ala Ser Val Phe Val Asn
685 690 695 700

Val Thr Asp Pro Ser Gln Val Ser His Gly Thr Gly Phe Thr Ser Phe
705 710 715

Gly Leu Leu Lys Leu Glu
720

<210> 21
<211> 728
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
HIV-human fusion construct

<220>
<221> SIGNAL
<222> (1)..(20)
<223> Synthetic secretory signal peptide

<220>
<221> DOMAIN
<222> (21)..(513)
<223> HIV gp120 domain with ProAspPro linker

<220>
<221> BINDING
<222> (514)..(728)
<223> CD154 extracellular domain long form amino acids 48(Arg) to
261(Leu) + Glu binds CD40

<400> 21
Met Leu Tyr Thr Ser Gln Leu Leu Gly Leu Leu Leu Phe Trp Ile Ser
-20 -15 -10 -5

Ala Ser Arg Ser Met Leu Leu Gly Ile Leu Met Ile Cys Ser Ala Thr
-1 1 5 10

Glu Lys Leu Trp Val Thr Val Tyr Tyr Gly Val Pro Val Trp Arg Glu
15 20 25

Ala Thr Thr Thr Leu Phe Cys Ala Ser Asp Ala Lys Ala Tyr Asp Thr
30 35 40

Glu Val His Asn Val Trp Ala Thr His Ala Cys Val Pro Thr Asp Pro
45 50 55 60

Asn Pro Gln Glu Val Val Leu Gly Asn Val Thr Glu Asn Phe Asn Met
65 70 75

Trp	Lys	Asn	Asn	Met	Val	Asp	Gln	Met	His	Glu	Asp	Ile	Ile	Ser	Leu	80	85	90	
Trp	Asp	Glu	Ser	Leu	Lys	Pro	Cys	Val	Lys	Leu	Thr	Pro	Leu	Cys	Val	95	100	105	
Thr	Leu	Asn	Cys	Thr	Asn	Leu	Asn	Ile	Thr	Lys	Asn	Thr	Thr	Asn	Pro	110	115	120	
Thr	Ser	Ser	Ser	Trp	Gly	Met	Met	Glu	Lys	Gly	Glu	Ile	Lys	Asn	Cys	125	130	135	140
Ser	Phe	Tyr	Ile	Thr	Thr	Ser	Ile	Arg	Asn	Lys	Val	Lys	Lys	Glu	Tyr	145	150	155	
Ala	Leu	Phe	Asn	Arg	Leu	Asp	Val	Val	Pro	Ile	Glu	Asn	Thr	Asn	Asn	160	165	170	
Thr	Lys	Tyr	Arg	Leu	Ile	Ser	Cys	Asn	Thr	Ser	Val	Ile	Thr	Gln	Ala	175	180	185	
Cys	Pro	Lys	Val	Ser	Phe	Gln	Pro	Ile	Pro	Ile	His	Tyr	Cys	Val	Pro	190	195	200	
Ala	Gly	Phe	Ala	Met	Leu	Lys	Cys	Asn	Asn	Lys	Thr	Phe	Asn	Gly	Ser	205	210	215	220
Gly	Pro	Cys	Thr	Asn	Val	Ser	Thr	Val	Gln	Cys	Thr	His	Gly	Ile	Arg	225	230	235	
Pro	Val	Val	Ser	Thr	Gln	Leu	Leu	Leu	Asn	Gly	Ser	Leu	Ala	Glu	Glu	240	245	250	
Asp	Ile	Val	Ile	Arg	Ser	Glu	Asn	Phe	Thr	Asp	Asn	Ala	Lys	Thr	Ile	255	260	265	
Ile	Val	Gln	Leu	Asn	Glu	Ser	Val	Val	Ile	Asn	Cys	Thr	Arg	Pro	Asn	270	275	280	
Asn	Asn	Thr	Arg	Arg	Arg	Leu	Ser	Ile	Gly	Pro	Gly	Arg	Ala	Phe	Tyr	285	290	295	300
Ala	Arg	Arg	Asn	Ile	Ile	Gly	Asp	Ile	Arg	Gln	Ala	His	Cys	Asn	Ile	305	310	315	
Ser	Arg	Ala	Lys	Trp	Asn	Asn	Thr	Leu	Gln	Gln	Ile	Val	Ile	Lys	Leu	320	325	330	
Arg	Glu	Lys	Phe	Arg	Asn	Lys	Thr	Ile	Ala	Phe	Asn	Gln	Ser	Ser	Gly	335	340	345	
Gly	Asp	Pro	Glu	Ile	Val	Met	His	Ser	Phe	Asn	Cys	Gly	Gly	Glu	Phe	350	355	360	
Phe	Tyr	Cys	Asn	Thr	Ala	Gln	Leu	Phe	Asn	Ser	Thr	Trp	Asn	Val	Thr	365	370	375	380

Gly Gly Thr Asn Gly Thr Glu Gly Asn Asp Ile Ile Thr Leu Gln Cys
 385 390 395
 Arg Ile Lys Gln Ile Ile Asn Met Trp Gln Lys Val Gly Lys Ala Met
 400 405 410
 Tyr Ala Pro Pro Ile Thr Gly Gln Ile Arg Cys Ser Ser Asn Ile Thr
 415 420 425
 Gly Leu Leu Leu Thr Arg Asp Gly Gly Asn Ser Thr Glu Thr Glu Thr
 430 435 440
 Glu Ile Phe Arg Pro Gly Gly Gly Asp Met Arg Asp Asn Trp Arg Ser
 445 450 455 460
 Glu Leu Tyr Lys Tyr Lys Val Val Arg Ile Glu Pro Ile Gly Val Ala
 465 470 475
 Pro Thr Arg Ala Lys Arg Arg Thr Val Gln Arg Glu Lys Arg Pro Asp
 480 485 490
 Pro Arg Arg Leu Asp Lys Ile Glu Asp Glu Arg Asn Leu His Glu Asp
 495 500 505
 Phe Val Phe Met Lys Thr Ile Gln Arg Cys Asn Thr Gly Glu Arg Ser
 510 515 520
 Leu Ser Leu Leu Asn Cys Glu Glu Ile Lys Ser Gln Phe Glu Gly Phe
 525 530 535 540
 Val Lys Asp Ile Met Leu Asn Lys Glu Glu Thr Lys Lys Glu Asn Ser
 545 550 555
 Phe Glu Met Gln Lys Gly Asp Gln Asn Pro Gln Ile Ala Ala His Val
 560 565 570
 Ile Ser Glu Ala Ser Ser Lys Thr Thr Ser Val Leu Gln Trp Ala Glu
 575 580 585
 Lys Gly Tyr Tyr Thr Met Ser Asn Asn Leu Val Thr Leu Glu Asn Gly
 590 595 600
 Lys Gln Leu Thr Val Lys Arg Gln Gly Leu Tyr Tyr Ile Tyr Ala Gln
 605 610 615 620
 Val Thr Phe Cys Ser Asn Arg Glu Ala Ser Ser Gln Ala Pro Phe Ile
 625 630 635
 Ala Ser Leu Cys Leu Lys Ser Pro Gly Arg Phe Glu Arg Ile Leu Leu
 640 645 650
 Arg Ala Ala Asn Thr His Ser Ser Ala Lys Pro Cys Gly Gln Gln Ser
 655 660 665
 Ile His Leu Gly Gly Val Phe Glu Leu Gln Pro Gly Ala Ser Val Phe
 670 675 680

Val Asn Val Thr Asp Pro Ser Gln Val Ser His Gly Thr Gly Phe Thr
685 690 695 700

Ser Phe Gly Leu Leu Lys Leu Glu
705

<210> 22

<211> 682

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
HIV-human fusion construct

<220>

<221> SIGNAL

<222> (1)..(20)

<223> Synthetic secretory signal peptide

<220>

<221> DOMAIN

<222> (21)..(525)

<223> HIV gp120 domain with (Gly4Ser)3 linker

<220>

<221> BINDING

<222> (528)..(682)

<223> CD154 extracellular domain long form amino acids 108(Glu) to
261(Leu) + Glu binds CD40

<400> 22

Met Leu Tyr Thr Ser Gln Leu Leu Gly Leu Leu Leu Phe Trp Ile Ser
-20 -15 -10 -5

Ala Ser Arg Ser Met Leu Leu Gly Ile Leu Met Ile Cys Ser Ala Thr
-1 1 5 10

Glu Lys Leu Trp Val Thr Val Tyr Tyr Gly Val Pro Val Trp Arg Glu
15 20 25

Ala Thr Thr Thr Leu Phe Cys Ala Ser Asp Ala Lys Ala Tyr Asp Thr
30 35 40

Glu Val His Asn Val Trp Ala Thr His Ala Cys Val Pro Thr Asp Pro
45 50 55 60

Asn Pro Gln Glu Val Val Leu Gly Asn Val Thr Glu Asn Phe Asn Met
65 70 75

Trp Lys Asn Asn Met Val Asp Gln Met His Glu Asp Ile Ile Ser Leu
80 85 90

Trp	Asp	Glu	Ser	Leu	Lys	Pro	Cys	Val	Lys	Leu	Thr	Pro	Leu	Cys	Val	95	100	105
Thr	Leu	Asn	Cys	Thr	Asn	Leu	Asn	Ile	Thr	Lys	Asn	Thr	Thr	Asn	Pro	110	115	120
Thr	Ser	Ser	Ser	Trp	Gly	Met	Met	Glu	Lys	Gly	Glu	Ile	Lys	Asn	Cys	125	130	135
Ser	Phe	Tyr	Ile	Thr	Thr	Ser	Ile	Arg	Asn	Lys	Val	Lys	Lys	Glu	Tyr	145	150	155
Ala	Leu	Phe	Asn	Arg	Leu	Asp	Val	Val	Pro	Ile	Glu	Asn	Thr	Asn	Asn	160	165	170
Thr	Lys	Tyr	Arg	Leu	Ile	Ser	Cys	Asn	Thr	Ser	Val	Ile	Thr	Gln	Ala	175	180	185
Cys	Pro	Lys	Val	Ser	Phe	Gln	Pro	Ile	Pro	Ile	His	Tyr	Cys	Val	Pro	190	195	200
Ala	Gly	Phe	Ala	Met	Leu	Lys	Cys	Asn	Asn	Lys	Thr	Phe	Asn	Gly	Ser	205	210	215
Gly	Pro	Cys	Thr	Asn	Val	Ser	Thr	Val	Gln	Cys	Thr	His	Gly	Ile	Arg	225	230	235
Pro	Val	Val	Ser	Thr	Gln	Leu	Leu	Leu	Asn	Gly	Ser	Leu	Ala	Glu	Glu	240	245	250
Asp	Ile	Val	Ile	Arg	Ser	Glu	Asn	Phe	Thr	Asp	Asn	Ala	Lys	Thr	Ile	255	260	265
Ile	Val	Gln	Leu	Asn	Glu	Ser	Val	Val	Ile	Asn	Cys	Thr	Arg	Pro	Asn	270	275	280
Asn	Asn	Thr	Arg	Arg	Arg	Leu	Ser	Ile	Gly	Pro	Gly	Arg	Ala	Phe	Tyr	285	290	295
Ala	Arg	Arg	Asn	Ile	Ile	Gly	Asp	Ile	Arg	Gln	Ala	His	Cys	Asn	Ile	305	310	315
Ser	Arg	Ala	Lys	Trp	Asn	Asn	Thr	Leu	Gln	Gln	Ile	Val	Ile	Lys	Leu	320	325	330
Arg	Glu	Lys	Phe	Arg	Asn	Lys	Thr	Ile	Ala	Phe	Asn	Gln	Ser	Ser	Gly	335	340	345
Gly	Asp	Pro	Glu	Ile	Val	Met	His	Ser	Phe	Asn	Cys	Gly	Gly	Glu	Phe	350	355	360
Phe	Tyr	Cys	Asn	Thr	Ala	Gln	Leu	Phe	Asn	Ser	Thr	Trp	Asn	Val	Thr	365	370	375
Gly	Gly	Thr	Asn	Gly	Thr	Glu	Gly	Asn	Asp	Ile	Ile	Thr	Leu	Gln	Cys	385	390	395

Arg	Ile	Lys	Gln	Ile	Ile	Asn	Met	Trp	Gln	Lys	Val	Gly	Lys	Ala	Met
			400					405					410		
Tyr	Ala	Pro	Pro	Ile	Thr	Gly	Gln	Ile	Arg	Cys	Ser	Ser	Asn	Ile	Thr
		415					420					425			
Gly	Leu	Leu	Leu	Thr	Arg	Asp	Gly	Gly	Asn	Ser	Thr	Glu	Thr	Glu	Thr
	430					435					440				
Glu	Ile	Phe	Arg	Pro	Gly	Gly	Gly	Asp	Met	Arg	Asp	Asn	Trp	Arg	Ser
445					450					455					460
Glu	Leu	Tyr	Lys	Tyr	Lys	Val	Val	Arg	Ile	Glu	Pro	Ile	Gly	Val	Ala
				465					470					475	
Pro	Thr	Arg	Ala	Lys	Arg	Arg	Thr	Val	Gln	Arg	Glu	Lys	Arg	Gly	Gly
			480					485					490		
Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Asp	Pro	Glu
		495					500					505			
Asn	Ser	Phe	Glu	Met	Gln	Lys	Gly	Asp	Gln	Asn	Pro	Gln	Ile	Ala	Ala
	510					515					520				
His	Val	Ile	Ser	Glu	Ala	Ser	Ser	Lys	Thr	Thr	Ser	Val	Leu	Gln	Trp
525					530					535					540
Ala	Glu	Lys	Gly	Tyr	Tyr	Thr	Met	Ser	Asn	Asn	Leu	Val	Thr	Leu	Glu
				545					550					555	
Asn	Gly	Lys	Gln	Leu	Thr	Val	Lys	Arg	Gln	Gly	Leu	Tyr	Tyr	Ile	Tyr
			560					565					570		
Ala	Gln	Val	Thr	Phe	Cys	Ser	Asn	Arg	Glu	Ala	Ser	Ser	Gln	Ala	Pro
		575					580					585			
Phe	Ile	Ala	Ser	Leu	Cys	Leu	Lys	Ser	Pro	Gly	Arg	Phe	Glu	Arg	Ile
	590					595					600				
Leu	Leu	Arg	Ala	Ala	Asn	Thr	His	Ser	Ser	Ala	Lys	Pro	Cys	Gly	Gln
605					610					615					620
Gln	Ser	Ile	His	Leu	Gly	Gly	Val	Phe	Glu	Leu	Gln	Pro	Gly	Ala	Ser
				625					630					635	
Val	Phe	Val	Asn	Val	Thr	Asp	Pro	Ser	Gln	Val	Ser	His	Gly	Thr	Gly
			640					645					650		
Phe	Thr	Ser	Phe	Gly	Leu	Leu	Lys	Leu	Glu						
		655					660								

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<210> 23
<211> 668
<212> PRT
<213> Artificial Sequence
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<220>

<223> Description of Artificial Sequence: Synthetic
HIV-human fusion construct

<220>

<221> SIGNAL

<222> (1)..(20)

<223> Synthetic secretory signal peptide

<220>

<221> DOMAIN

<222> (21)..(513)

<223> HIV gp120 domain with ProAspPro linker

<220>

<221> BINDING

<222> (514)..(668)

<223> CD154 extracellular domain long form amino acids 108(Glu) to
261(Leu) + Glu binds CD40

<400> 23

Met Leu Tyr Thr Ser Gln Leu Leu Gly Leu Leu Leu Phe Trp Ile Ser
-20 -15 -10 -5

Ala Ser Arg Ser Met Leu Leu Gly Ile Leu Met Ile Cys Ser Ala Thr
-1 1 5 10

Glu Lys Leu Trp Val Thr Val Tyr Tyr Gly Val Pro Val Trp Arg Glu
15 20 25

Ala Thr Thr Thr Leu Phe Cys Ala Ser Asp Ala Lys Ala Tyr Asp Thr
30 35 40

Glu Val His Asn Val Trp Ala Thr His Ala Cys Val Pro Thr Asp Pro
45 50 55 60

Asn Pro Gln Glu Val Val Leu Gly Asn Val Thr Glu Asn Phe Asn Met
65 70 75

Trp Lys Asn Asn Met Val Asp Gln Met His Glu Asp Ile Ile Ser Leu
80 85 90

Trp Asp Glu Ser Leu Lys Pro Cys Val Lys Leu Thr Pro Leu Cys Val
95 100 105

Thr Leu Asn Cys Thr Asn Leu Asn Ile Thr Lys Asn Thr Thr Asn Pro
110 115 120

Thr Ser Ser Ser Trp Gly Met Met Glu Lys Gly Glu Ile Lys Asn Cys
125 130 135 140

Ser Phe Tyr Ile Thr Thr Ser Ile Arg Asn Lys Val Lys Lys Glu Tyr
145 150 155

Ala Leu Phe Asn Arg Leu Asp Val Val Pro Ile Glu Asn Thr Asn Asn
160 165 170

Thr	Lys	Tyr	Arg	Leu	Ile	Ser	Cys	Asn	Thr	Ser	Val	Ile	Thr	Gln	Ala		
		175					180					185					
Cys	Pro	Lys	Val	Ser	Phe	Gln	Pro	Ile	Pro	Ile	His	Tyr	Cys	Val	Pro		
	190					195					200						
Ala	Gly	Phe	Ala	Met	Leu	Lys	Cys	Asn	Asn	Lys	Thr	Phe	Asn	Gly	Ser		
205					210					215					220		
Gly	Pro	Cys	Thr	Asn	Val	Ser	Thr	Val	Gln	Cys	Thr	His	Gly	Ile	Arg		
				225					230					235			
Pro	Val	Val	Ser	Thr	Gln	Leu	Leu	Leu	Asn	Gly	Ser	Leu	Ala	Glu	Glu		
			240					245					250				
Asp	Ile	Val	Ile	Arg	Ser	Glu	Asn	Phe	Thr	Asp	Asn	Ala	Lys	Thr	Ile		
	255						260					265					
Ile	Val	Gln	Leu	Asn	Glu	Ser	Val	Val	Ile	Asn	Cys	Thr	Arg	Pro	Asn		
	270					275					280						
Asn	Asn	Thr	Arg	Arg	Arg	Leu	Ser	Ile	Gly	Pro	Gly	Arg	Ala	Phe	Tyr		
285					290					295					300		
Ala	Arg	Arg	Asn	Ile	Ile	Gly	Asp	Ile	Arg	Gln	Ala	His	Cys	Asn	Ile		
			305					310					315				
Ser	Arg	Ala	Lys	Trp	Asn	Asn	Thr	Leu	Gln	Gln	Ile	Val	Ile	Lys	Leu		
			320					325					330				
Arg	Glu	Lys	Phe	Arg	Asn	Lys	Thr	Ile	Ala	Phe	Asn	Gln	Ser	Ser	Gly		
	335						340					345					
Gly	Asp	Pro	Glu	Ile	Val	Met	His	Ser	Phe	Asn	Cys	Gly	Gly	Glu	Phe		
	350					355					360						
Phe	Tyr	Cys	Asn	Thr	Ala	Gln	Leu	Phe	Asn	Ser	Thr	Trp	Asn	Val	Thr		
365					370				375						380		
Gly	Gly	Thr	Asn	Gly	Thr	Glu	Gly	Asn	Asp	Ile	Ile	Thr	Leu	Gln	Cys		
			385					390						395			
Arg	Ile	Lys	Gln	Ile	Ile	Asn	Met	Trp	Gln	Lys	Val	Gly	Lys	Ala	Met		
			400				405						410				
Tyr	Ala	Pro	Pro	Ile	Thr	Gly	Gln	Ile	Arg	Cys	Ser	Ser	Asn	Ile	Thr		
	415						420					425					
Gly	Leu	Leu	Leu	Thr	Arg	Asp	Gly	Gly	Asn	Ser	Thr	Glu	Thr	Glu	Thr		
	430					435					440						
Glu	Ile	Phe	Arg	Pro	Gly	Gly	Gly	Asp	Met	Arg	Asp	Asn	Trp	Arg	Ser		
445					450				455					460			
Glu	Leu	Tyr	Lys	Tyr	Lys	Val	Val	Arg	Ile	Glu	Pro	Ile	Gly	Val	Ala		
			465					470					475				

Pro Thr Arg Ala Lys Arg Arg Thr Val Gln Arg Glu Lys Arg Pro Asp
 480 485 490
 Pro Glu Asn Ser Phe Glu Met Gln Lys Gly Asp Gln Asn Pro Gln Ile
 495 500 505
 Ala Ala His Val Ile Ser Glu Ala Ser Ser Lys Thr Thr Ser Val Leu
 510 515 520
 Gln Trp Ala Glu Lys Gly Tyr Tyr Thr Met Ser Asn Asn Leu Val Thr
 525 530 535 540
 Leu Glu Asn Gly Lys Gln Leu Thr Val Lys Arg Gln Gly Leu Tyr Tyr
 545 550 555
 Ile Tyr Ala Gln Val Thr Phe Cys Ser Asn Arg Glu Ala Ser Ser Gln
 560 565 570
 Ala Pro Phe Ile Ala Ser Leu Cys Leu Lys Ser Pro Gly Arg Phe Glu
 575 580 585
 Arg Ile Leu Leu Arg Ala Ala Asn Thr His Ser Ser Ala Lys Pro Cys
 590 595 600
 Gly Gln Gln Ser Ile His Leu Gly Gly Val Phe Glu Leu Gln Pro Gly
 605 610 615 620
 Ala Ser Val Phe Val Asn Val Thr Asp Pro Ser Gln Val Ser His Gly
 625 630 635
 Thr Gly Phe Thr Ser Phe Gly Leu Leu Lys Leu Glu
 640 645

<210> 24

<211> 294

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
HIV-human fusion construct

<220>

<221> SIGNAL

<222> (1)..(20)

<223> Synthetic secretory signal peptide

<220>

<221> DOMAIN

<222> (21)..(77)

<223> HIV gp120 V3 loop with (Gly4Ser)3 linker

<220>

<221> BINDING

<222> (80)..(294)

<223> CD154 extracellular domain long form amino acids 48(Arg) to 261(Leu) + Glu binds CD40

<400> 24

Met Leu Tyr Thr Ser Gln Leu Leu Gly Leu Leu Leu Phe Trp Ile Ser
 -20 -15 -10 -5

Ala Ser Arg Ser Val Val Ile Asn Cys Thr Arg Pro Asn Asn Asn Thr
 -1 1 5 10

Arg Arg Arg Leu Ser Ile Gly Pro Gly Arg Ala Phe Tyr Ala Arg Arg
 15 20 25

Asn Ile Ile Gly Asp Ile Arg Gln Ala His Cys Asn Ile Ser Gly Gly
 30 35 40

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Pro Arg
 45 50 55 60

Arg Leu Asp Lys Ile Glu Asp Glu Arg Asn Leu His Glu Asp Phe Val
 65 70 75

Phe Met Lys Thr Ile Gln Arg Cys Asn Thr Gly Glu Arg Ser Leu Ser
 80 85 90

Leu Leu Asn Cys Glu Glu Ile Lys Ser Gln Phe Glu Gly Phe Val Lys
 95 100 105

Asp Ile Met Leu Asn Lys Glu Glu Thr Lys Lys Glu Asn Ser Phe Glu
 110 115 120

Met Gln Lys Gly Asp Gln Asn Pro Gln Ile Ala Ala His Val Ile Ser
 125 130 135 140

Glu Ala Ser Ser Lys Thr Thr Ser Val Leu Gln Trp Ala Glu Lys Gly
 145 150 155

Tyr Tyr Thr Met Ser Asn Asn Leu Val Thr Leu Glu Asn Gly Lys Gln
 160 165 170

Leu Thr Val Lys Arg Gln Gly Leu Tyr Tyr Ile Tyr Ala Gln Val Thr
 175 180 185

Phe Cys Ser Asn Arg Glu Ala Ser Ser Gln Ala Pro Phe Ile Ala Ser
 190 195 200

Leu Cys Leu Lys Ser Pro Gly Arg Phe Glu Arg Ile Leu Leu Arg Ala
 205 210 215 220

Ala Asn Thr His Ser Ser Ala Lys Pro Cys Gly Gln Gln Ser Ile His
 225 230 235

Leu Gly Gly Val Phe Glu Leu Gln Pro Gly Ala Ser Val Phe Val Asn
 240 245 250

Gly Leu Leu Lys Leu Glu
270

```
<210> 25
<211> 280
<212> PRT
<213> Artificial Sequence
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<220>
<223> Description of Artificial Sequence: Synthetic
HIV-human fusion construct

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<220>
<221> SIGNAL
<222> (1)..(20)
<223> Synthetic secretory signal peptide
```

```
<220>
<221> DOMAIN
<222> (21)..(65)
<223> HIV gp120 V3 loop with ProAspPro linker
```

```
<220>
<221> BINDING
<222> (66)..(280)
<223> CD154 extracellular domain long form amino acids 48(Arg) to
      261(Leu) + Glu binds CD40
```

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<400> 25
Met Leu Tyr Thr Ser Gln Leu Leu Gly Leu Leu Leu Phe Trp Ile Ser
-20                      -15                      -10                      -5

Ala Ser Arg Ser Val Val Ile Asn Cys Thr Arg Pro Asn Asn Asn Thr
      -1      1                      5                      10

Arg Arg Arg Leu Ser Ile Gly Pro Gly Arg Ala Phe Tyr Ala Arg Arg
      15                      20                      25

Asn Ile Ile Gly Asp Ile Arg Gln Ala His Cys Asn Ile Ser Pro Asp
      30                      35                      40

Pro Arg Arg Leu Asp Lys Ile Glu Asp Glu Arg Asn Leu His Glu Asp
  45                      50                      55                      60

Phe Val Phe Met Lys Thr Ile Gln Arg Cys Asn Thr Gly Glu Arg Ser
      65                      70                      75

Leu Ser Leu Leu Asn Cys Glu Glu Ile Lys Ser Gln Phe Glu Gly Phe
      80                      85                      90

```

```

Val Lys Asp Ile Met Leu Asn Lys Glu Glu Thr Lys Lys Glu Asn Ser
    95                      100                      105

Phe Glu Met Gln Lys Gly Asp Gln Asn Pro Gln Ile Ala Ala His Val
    110                      115                      120

Ile Ser Glu Ala Ser Ser Lys Thr Thr Ser Val Leu Gln Trp Ala Glu
    125                      130                      135                      140

Lys Gly Tyr Tyr Thr Met Ser Asn Asn Leu Val Thr Leu Glu Asn Gly
                      145                      150                      155

Lys Gln Leu Thr Val Lys Arg Gln Gly Leu Tyr Tyr Ile Tyr Ala Gln
                      160                      165                      170

Val Thr Phe Cys Ser Asn Arg Glu Ala Ser Ser Gln Ala Pro Phe Ile
                      175                      180                      185

Ala Ser Leu Cys Leu Lys Ser Pro Gly Arg Phe Glu Arg Ile Leu Leu
    190                      195                      200

Arg Ala Ala Asn Thr His Ser Ser Ala Lys Pro Cys Gly Gln Gln Ser
    205                      210                      215                      220

Ile His Leu Gly Gly Val Phe Glu Leu Gln Pro Gly Ala Ser Val Phe
                      225                      230                      235

Val Asn Val Thr Asp Pro Ser Gln Val Ser His Gly Thr Gly Phe Thr
                      240                      245                      250

Ser Phe Gly Leu Leu Lys Leu Glu
    255                      260

```

```

<210> 26
<211> 234
<212> PRT
<213> Artificial Sequence

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<220>
<223> Description of Artificial Sequence: Synthetic
      HIV-human fusion construct

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<220>
<221> SIGNAL
<222> (1)..(20)
<223> Synthetic secretory signal peptide

```

```

<220>
<221> DOMAIN
<222> (21)..(77)
<223> HIV gp120 V3 loop with (Gly4Ser)3 linker

```

```

<220>
<221> BINDING

```


<222> (80)..(234)

<223> CD154 extracellular domain long form amino acids 108(Glu) to
261(Leu) + Glu binds CD40

<400> 26

Met Leu Tyr Thr Ser Gln Leu Leu Gly Leu Leu Leu Phe Trp Ile Ser
-20 -15 -10 -5

Ala Ser Arg Ser Val Val Ile Asn Cys Thr Arg Pro Asn Asn Asn Thr
-1 1 5 10

Arg Arg Arg Leu Ser Ile Gly Pro Gly Arg Ala Phe Tyr Ala Arg Arg
15 20 25

Asn Ile Ile Gly Asp Ile Arg Gln Ala His Cys Asn Ile Ser Gly Gly
30 35 40

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Pro Glu
45 50 55 60

Asn Ser Phe Glu Met Gln Lys Gly Asp Gln Asn Pro Gln Ile Ala Ala
65 70 75

His Val Ile Ser Glu Ala Ser Ser Lys Thr Thr Ser Val Leu Gln Trp
80 85 90

Ala Glu Lys Gly Tyr Tyr Thr Met Ser Asn Asn Leu Val Thr Leu Glu
95 100 105

Asn Gly Lys Gln Leu Thr Val Lys Arg Gln Gly Leu Tyr Tyr Ile Tyr
110 115 120

Ala Gln Val Thr Phe Cys Ser Asn Arg Glu Ala Ser Ser Gln Ala Pro
125 130 135 140

Phe Ile Ala Ser Leu Cys Leu Lys Ser Pro Gly Arg Phe Glu Arg Ile
145 150 155

Leu Leu Arg Ala Ala Asn Thr His Ser Ser Ala Lys Pro Cys Gly Gln
160 165 170

Gln Ser Ile His Leu Gly Gly Val Phe Glu Leu Gln Pro Gly Ala Ser
175 180 185

Val Phe Val Asn Val Thr Asp Pro Ser Gln Val Ser His Gly Thr Gly
190 195 200

Phe Thr Ser Phe Gly Leu Leu Lys Leu Glu
205 210

<210> 27

<211> 220

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
HIV-human fusion construct

<220>

<221> SIGNAL

<222> (1)..(20)

<223> Synthetic secretory signal peptide

<220>

<221> DOMAIN

<222> (21)..(65)

<223> HIV gp120 V3 loop with ProAspPro linker

<220>

<221> BINDING

<222> (66)..(220)

<223> CD154 extracellular domain long form amino acids 108(Glu) to
261(Leu) + Glu binds CD40

<400> 27

Met Leu Tyr Thr Ser Gln Leu Leu Gly Leu Leu Leu Phe Trp Ile Ser
-20 -15 -10 -5

Ala Ser Arg Ser Val Val Ile Asn Cys Thr Arg Pro Asn Asn Asn Thr
-1 1 5 10

Arg Arg Arg Leu Ser Ile Gly Pro Gly Arg Ala Phe Tyr Ala Arg Arg
15 20 25

Asn Ile Ile Gly Asp Ile Arg Gln Ala His Cys Asn Ile Ser Pro Asp
30 35 40

Pro Glu Asn Ser Phe Glu Met Gln Lys Gly Asp Gln Asn Pro Gln Ile
45 50 55 60

Ala Ala His Val Ile Ser Glu Ala Ser Ser Lys Thr Thr Ser Val Leu
65 70 75

Gln Trp Ala Glu Lys Gly Tyr Tyr Thr Met Ser Asn Asn Leu Val Thr
80 85 90

Leu Glu Asn Gly Lys Gln Leu Thr Val Lys Arg Gln Gly Leu Tyr Tyr
95 100 105

Ile Tyr Ala Gln Val Thr Phe Cys Ser Asn Arg Glu Ala Ser Ser Gln
110 115 120

Ala Pro Phe Ile Ala Ser Leu Cys Leu Lys Ser Pro Gly Arg Phe Glu
125 130 135 140

Arg Ile Leu Leu Arg Ala Ala Asn Thr His Ser Ser Ala Lys Pro Cys
145 150 155

Gly Gln Gln Ser Ile His Leu Gly Gly Val Phe Glu Leu Gln Pro Gly
160 165 170

Thr Gly Phe Thr Ser Phe Gly Leu Leu Lys Leu Glu
190 195 200

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<210> 28
<211> 6
<212> PRT
<213> Human immunodeficiency virus type 1
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<400> 28
Gly Pro Gly Arg Ala Phe
1 5

```
<210> 29
<211> 15
<212> PRT
<213> Artificial Sequence
```

<220>
<223> Description of Artificial Sequence: Linker peptide

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<400> 29
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
  1             5             10            15
```